

AMENDMENTS TO THE CLAIMS

Listing of Claims:

1. (Currently amended) A method for identifying herbicidally active substances comprising

a) identifying a substance which influences ~~selecting a substance which reduces or blocks~~

i) the expression of a nucleic acid or gene or the activity of the gene product of a nucleic acid or a gene, wherein the nucleic acid or gene comprises:

aa) a the nucleic acid sequence with the sequence shown in of SEQ ID NO: 1; SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49 or SEQ ID NO: 51;

bb) a nucleic acid sequence which can be derived from encoding a polypeptide comprising the amino acid sequence[[s]] shown in of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50 or SEQ ID NO: 52 by backtranslation owing to the degeneracy of the genetic code;

cc) a nucleic acid sequence which is a derivative or a fragment of the nucleic acid sequences shown in having at least 90% homology with SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49 or SEQ ID NO: 51 and which has at least 60% homology at the nucleic acid level,

dd) a nucleic acid sequence which encodes derivatives or fragments of the a polypeptide[[s]] comprising an amino acid sequence having at least 90% homology with the amino acid sequence[[s]] shown in of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18,

SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50 or SEQ ID NO: 52 and which have at least 50% homology at the amino acid level;

ee) a nucleic acid sequence which encodes a fragment or an epitope of a polypeptide which binds specifically to an antibody, the antibody specifically binding to a polypeptide which is encoded by the sequence shown in SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49 or SEQ ID NO: 51;

ff) a nucleic acid sequence which encodes a fragment of [[a]] the nucleic acid shown in aa) and which has a translation releasing factor activity; a cobalamin synthase activity; an arginyl-tRNA synthase activity; an RNA helicase activity; a GTP binding protein activity; a pseudouridylate synthase activity; an adenylate kinase activity; a preprotein translocase secA precursor protein activity; a DCL protein activity; an arginine-tRNA ligase activity; a plastidial glutathione reductase activity; a transcription factor sigma activity; a calmodulin activity; an INT6 activity; a helicase YGL150e activity; an RNA binding activity; a heat shock transcription factor activity; a chloroplastidial DNA-nucleoid binding activity or a Met2 type cytosine-DNA methyltransferase activity; and/or or

gg) a nucleic acid sequence which encodes derivatives of the a polypeptide[[s]] having at least 90% homology with the amino acid sequence[[s]] shown in of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50 or SEQ ID NO: 52 and which has at least 20% homology at the amino acid level and has an equivalent biological activity;

or

ii) the expression of an amino acid sequence, or the activity of an amino acid sequence, wherein the ~~gene product comprises an~~ amino acid sequence which is encoded by [[a]] the nucleic acid sequence of aa), bb), cc), dd), ee), ff), to or gg); and

b) selecting a substance which reduces or blocks the expression of said nucleic acid or gene or amino acid sequence, or the activity of the gene product of said nucleic acid or gene, or the activity of said amino acid sequence, wherein the selected substance is a low-molecular weight substance.

2. (Currently amended) The method of claim 1, wherein the expression of the nucleic acid or gene, or the activity of the ~~nucleic acid or the gene product of the nucleic acid or gene, or the~~ activity of the amino acid sequence is reduced or blocked by reducing or blocking the

- a) transcription,
- b) translation,
- c) processing and/or
- d) modification

of the nucleic acid sequence or amino acid sequence in claim 1.

3. (Cancelled)

4. (Previously presented) The method of claim 1, wherein the identification of the substances is carried out in a high-throughput screening (HTS).

5. (Currently amended) The method of claim 1, wherein the selected substance[[s]] are is applied to a plant in order to test the herbicidal activity of the substance[[s]] and the substance[[s]] which ~~show~~ shows herbicidal activity are is selected.

6. (Previously presented) The method of claim 1, wherein the method is carried out in an organism.

7. (Previously presented) The method of claim 6, wherein bacteria, yeasts, fungi or plants are used as the organism.

8. (Currently amended) The method of claim 1, wherein the method is carried out in an organism ~~which is~~ and the organism comprises a conditional or natural mutant of one of the sequences described in claim 1.

9-18. (Canceled).

19. (Withdrawn, currently amended) A method of identifying an antagonist of proteins which are encoded by a nucleic acid sequence as ~~claimed~~ described in claim [[9]] 1 comprising the following steps

- i) contacting cells which express the protein, or the protein, with a candidate substance;
- ii) testing the biological activity of the protein;
- iii) comparing the biological activity of the protein with a standard activity in the absence of the candidate substance, a reduced biological activity of the protein indicating that the candidate substance is an antagonist.

20. (Withdrawn) The method as claimed in claim 19, wherein the antagonist is applied to a plant to test its herbicidal activity, and those antagonists which show a herbicidal activity are selected.

21. (Withdrawn; currently amended) A method of controlling undesired vegetation, which comprises allowing a herbicidally active amount of [[a]] the substance identified by the method of claim 1 to act on plants and/or their environment.

22. (Withdrawn) A method for regulating the growth of a plant comprising using an antagonist identified by the method of claim 19.

23-24. (Cancelled)

25. (Withdrawn; currently amended) A method for generating transgenic plants which are resistant to substances found by the method of claim 1, which comprises overexpressing, in these plants, a nucleic acid[[s]] with the sequence[[s]] as described in claim 1.

26-30. (Cancelled)